



<110> Chen, Li Hw  
Meade, Harry M.

<130> 10275-134001

<140> US 09/175,683

<141> 1998-10-20

<150> US 60/085,649

<151> 1998-05-15

<150> US 60/062,592

<151> 1997-10-20

<160> 19

<170> FastSEQ for Windows Version 4.0

 $\langle 210 \rangle$  1

<211> 1065

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$ 

<223> altered MSP sequence; preferably, a bacterium, virus, or parasite

<221> CDS

<222> (1) ... (1065)

<400> 1

gcc gtc act ccc tcc gtc atc gat aac atc ctg tcc aag atc gag aac 48  
Ala Val Thr Pro Ser Val Ile Asp Asn Ile Leu Ser Lys Ile Glu Asn  
1 5 10 15

gag tac gag gtg ctg tac ctg aag ccg ctg gca ggg gtc tac cgg agc 96  
Glu Tyr Glu Val Leu Tyr Leu Lys Pro Leu Ala Gly Val Tyr Arg Ser  
20 25 30

ctg aag aag cag ctg gag aac aac gtg atg acc ttc aac gtg aac gtg 144  
Leu Lys Lys Gln Leu Glu Asn Asn Val Met Thr Phe Asn Val Asn Val  
35 40 45

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aag gat atc ctg aac agc cgg ttc aac aag cgg gag aac ttc aag aac      192
Lys Asp Ile Leu Asn Ser Arg Phe Asn Lys Arg Glu Asn Phe Lys Asn
      50                      55                      60

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gtg ctg gag agc gat ctg atc ccc tac aag gat ctg acc agc agc aac 240  
Val Leu Glu Ser Asp Leu Ile Pro Tyr Lys Asp Leu Thr Ser Ser Asn

65	70	75	80	
tac gtg gtc aag gat ccc tac aag ttc ctg aac aag gag aag aga gat				288
Tyr Val Val Lys Asp Pro Tyr Lys Phe Leu Asn Lys Glu Lys Arg Asp				
	85	90	95	
aag ttc ctg agc agt tac aac tac atc aag gat agc att gat acc gat				336
Lys Phe Leu Ser Ser Tyr Asn Tyr Ile Lys Asp Ser Ile Asp Thr Asp				
	100	105	110	
atc aac ttc gcc aac gat gtc ctg gga tac tac aag atc ctg tcc gag				384
Ile Asn Phe Ala Asn Asp Val Leu Gly Tyr Tyr Lys Ile Leu Ser Glu				
	115	120	125	
aag tac aag agc gat ctg gat tca atc aag aag tac atc aac gat aag				432
Lys Tyr Lys Ser Asp Leu Asp Ser Ile Lys Lys Tyr Ile Asn Asp Lys				
	130	135	140	
cag gga gag aac gag aag tac ctg ccc ttc ctg aac aac atc gag acc				480
Gln Gly Glu Asn Glu Lys Tyr Leu Pro Phe Leu Asn Asn Ile Glu Thr				
	145	150	155	160
ctg tac aag acc gtc aac gat aag att gat ctg ttc gtg atc cac ctg				528
Leu Tyr Lys Thr Val Asn Asp Lys Ile Asp Leu Phe Val Ile His Leu				
	165	170	175	
gag gcc aag gtc ctg aac tac aca tat gag aag agc aac gtg gag gtc				576
Glu Ala Lys Val Leu Asn Tyr Thr Tyr Glu Lys Ser Asn Val Glu Val				
	180	185	190	
aag atc aag gag ctg aat tac ctg aag acc atc cag gat aag ctg gcc				624
Lys Ile Lys Glu Leu Asn Tyr Leu Lys Thr Ile Gln Asp Lys Leu Ala				
	195	200	205	
gat ttc aag aag aac aac aac ttc gtc ggg atc gcc gat ctg agc acc				672
Asp Phe Lys Lys Asn Asn Asn Phe Val Gly Ile Ala Asp Leu Ser Thr				
	210	215	220	
gat tac aac cac aac aac ctg ctg acc aag ttc ctg agc acc ggt atg				720
Asp Tyr Asn His Asn Asn Leu Leu Thr Lys Phe Leu Ser Thr Gly Met				
	225	230	235	240
gtc ttc gaa aac ctg gcc aag acc gtc ctg agc aac ctg ctg gat ggg				768
Val Phe Glu Asn Leu Ala Lys Thr Val Leu Ser Asn Leu Leu Asp Gly				
	245	250	255	
aac ctg cag ggg atg ctg aac atc agc cag cac cag tgt gtg aag aag				816
Asn Leu Gln Gly Met Leu Asn Ile Ser Gln His Gln Cys Val Lys Lys				
	260	265	270	
cag tgt ccc cag aac agc ggg tgt ttc aga cac ctg gat gag aga gag				864
Gln Cys Pro Gln Asn Ser Gly Cys Phe Arg His Leu Asp Glu Arg Glu				
	275	280	285	
gag tgt aag tgt ctg ctg aac tac aag cag gaa ggt gat aag tgt gtg				912
Glu Cys Lys Cys Leu Leu Asn Tyr Lys Gln Glu Gly Asp Lys Cys Val				
	290	295	300	

gaa aac ccc aat cct act tgt aac gag aac aat ggt gga tgt gat gcc 960  
 Glu Asn Pro Asn Pro Thr Cys Asn Glu Asn Asn Gly Gly Cys Asp Ala  
 305 310 315 320

gat gcc aag tgt acc gag gag gat tca ggg agc aac ggg aag aag atc 1008  
 Asp Ala Lys Cys Thr Glu Glu Asp Ser Gly Ser Asn Gly Lys Lys Ile  
 325 330 335

acc tgt gag tgt acc aag cct gat tct tat cca ctg ttc gat ggt atc 1056  
 Thr Cys Glu Cys Thr Lys Pro Asp Ser Tyr Pro Leu Phe Asp Gly Ile  
 340 345 350

ttc tgt agt 1065  
 Phe Cys Ser  
 355

<210> 2

<211> 1088

<212> DNA

<213> Plasmodium falciparum

<220>

<221> CDS

<222> (1)...(1083) .

<400> 2

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 Ala Val Thr Pro Ser Val Ile Asp Asn Ile Leu Ser Lys Ile Glu Asn  
 1 5 10 15

gaa tat gag gtt tta tat tta aaa cct tta gca ggt gtt tat aga agt 96  
 Glu Tyr Glu Val Leu Tyr Leu Lys Pro Leu Ala Gly Val Tyr Arg Ser  
 20 25 30

tta aaa aaa caa tta gaa aat aac gtt atg aca ttt aat gtt aat gtt 144  
 Leu Lys Lys Gln Leu Glu Asn Asn Val Met Thr Phe Asn Val Asn Val  
 35 40 45

aag gat att tta aat tca cga ttt aat aaa cgt gaa aat ttc aaa aat 192  
 Lys Asp Ile Leu Asn Ser Arg Phe Asn Lys Arg Glu Asn Phe Lys Asn  
 50 55 60

gtt tta gaa tca gat tta att cca tat aaa gat tta aca tca agt aat 240  
 Val Leu Glu Ser Asp Leu Ile Pro Tyr Lys Asp Leu Thr Ser Ser Asn  
 65 70 75 80

tat gtt gtc aaa gat cca tat aaa ttt ctt aat aaa gaa aaa aga gat 288  
 Tyr Val Val Lys Asp Pro Tyr Lys Phe Leu Asn Lys Glu Lys Arg Asp  
 85 90 95

aaa ttc tta agc agt tat aat tat att aag gat tca ata gat acg gat 336  
 Lys Phe Leu Ser Ser Tyr Asn Tyr Ile Lys Asp Ser Ile Asp Thr Asp  
 100 105 110

ata aat ttt gca aat gat gtt ctt gga tat tat aaa ata tta tcc gaa 384

Ile Asn Phe Ala Asn Asp Val Leu Gly Tyr Tyr Lys Ile Leu Ser Glu	
115 120 125	
aaa tat aaa tca gat tta gat tca att aaa aaa tat atc aac gac aaa	432
Lys Tyr Lys Ser Asp Leu Asp Ser Ile Lys Lys Tyr Ile Asn Asp Lys	
130 135 140	
caa ggt gaa aat gag aaa tac ctt ccc ttt tta aac aat att gag acc	480
Gln Gly Glu Asn Glu Lys Tyr Leu Pro Phe Leu Asn Asn Ile Glu Thr	
145 150 155 160	
tta tat aaa aca gtt aat gat aaa att gat tta ttt gta att cat tta	528
Leu Tyr Lys Thr Val Asn Asp Lys Ile Asp Leu Phe Val Ile His Leu	
165 170 175	
gaa gca aaa gtt cta aat tat aca tat gag aaa tca aac gta gaa gtt	576
Glu Ala Lys Val Leu Asn Tyr Thr Tyr Glu Lys Ser Asn Val Glu Val	
180 185 190	
aaa ata aaa gaa ctt aat tac tta aaa aca att caa gac aaa ttg gca	624
Lys Ile Lys Glu Leu Asn Tyr Leu Lys Thr Ile Gln Asp Lys Leu Ala	
195 200 205	
gat ttt aaa aaa aat aac aat ttc gtt gga att gct gat tta tca aca	672
Asp Phe Lys Lys Asn Asn Asn Phe Val Gly Ile Ala Asp Leu Ser Thr	
210 215 220	
gat tat aac cat aat aac tta ttg aca aag ttc ctt agt aca ggt atg	720
Asp Tyr Asn His Asn Asn Leu Leu Thr Lys Phe Leu Ser Thr Gly Met	
225 230 235 240	
gtt ttt gaa aat ctt gct aaa acc gtt tta tct aat tta ctt gat gga	768
Val Phe Glu Asn Leu Ala Lys Thr Val Leu Ser Asn Leu Leu Asp Gly	
245 250 255	
aac ttg caa ggt atg tta aac att tca caa cac caa tgc gta aaa aaa	816
Asn Leu Gln Gly Met Leu Asn Ile Ser Gln His Gln Cys Val Lys Lys	
260 265 270	
caa tgt cca caa aat tct gga tgt ttc aga cat tta gat gaa aga gaa	864
Gln Cys Pro Gln Asn Ser Gly Cys Phe Arg His Leu Asp Glu Arg Glu	
275 280 285	
gaa tgt aaa tgt tta tta aat tac aaa caa gaa ggt gat aaa tgt gtt	912
Glu Cys Lys Cys Leu Leu Asn Tyr Lys Gln Glu Gly Asp Lys Cys Val	
290 295 300	
gaa aat cca aat cct act tgt aac gaa aat aat ggt gga tgt gat gca	960
Glu Asn Pro Asn Pro Thr Cys Asn Glu Asn Asn Gly Gly Cys Asp Ala	
305 310 315 320	
gat gcc aaa tgt acc gaa gaa gat tca ggt agc aac gga aag aaa atc	1008
Asp Ala Lys Cys Thr Glu Glu Asp Ser Gly Ser Asn Gly Lys Lys Ile	
325 330 335	
aca tgt gaa tgt act aaa cct gat tct tat cca ctt ttc gat ggt att	1056
Thr Cys Glu Cys Thr Lys Pro Asp Ser Tyr Pro Leu Phe Asp Gly Ile	



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<210> 7
<211> 31
<212> DNA
<213> Artificial Sequence
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&lt;220&gt;

&lt;223&gt; oligonucleotide for PCR

&lt;400&gt; 7

aatagatctg cagtaactcc ttccgtaatt g

31

&lt;210&gt; 8

&lt;211&gt; 1142

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> altered MSP sequence; preferably, a bacterium,  
virus, or parasite

&lt;221&gt; CDS

&lt;222&gt; (1)...(1142)

&lt;400&gt; 8

atg aag gtc ctc ata att gcc tgt ctg gtg gct ctg gcc att gca gcc 48

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1 5 10 15

gtc act ccc tcc gtc atc gat aac atc ctg tcc aag atc gag aac gag 96

Val Thr Pro Ser Val Ile Asp Asn Ile Leu Ser Lys Ile Glu Asn Glu  
20 25 30

tac gag gtg ctg tac ctg aag ccc ctg gca gga gtc tac agg agc ctg 144

Tyr Glu Val Leu Tyr Leu Lys Pro Leu Ala Gly Val Tyr Arg Ser Leu  
35 40 45

aag aag cag ctg gag aac aac gtg atg acc ttc aac gtg aac gtg aag 192

Lys Lys Gln Leu Glu Asn Asn Val Met Thr Phe Asn Val Asn Val Lys  
50 55 60

gat atc ctg aac agc agg ttc aac aag agg gag aac ttc aag aac gtg 240

Asp Ile Leu Asn Ser Arg Phe Asn Lys Arg Glu Asn Phe Lys Asn Val  
65 70 75 80

ctg gag agc gat ctg atc ccc tac aag gat ctg acc agc agc aac tac 288

Leu Glu Ser Asp Leu Ile Pro Tyr Lys Asp Leu Thr Ser Ser Asn Tyr  
85 90 95

gtg gtc aaa gat ccc tac aag ttc ctg aac aag gag aag aga gat aag 336

Val Val Lys Asp Pro Tyr Lys Phe Leu Asn Lys Glu Lys Arg Asp Lys  
100 105 110

ttc ctg agc agt tac aat tac atc aag gat agc att gac acc gat atc 384

Phe Leu Ser Ser Tyr Asn Tyr Ile Lys Asp Ser Ile Asp Thr Asp Ile  
115 120 125

aac ttc gcc aac gat gtc ctg gga tac tac aag atc ctg tcc gag aag 432

Asn Phe Ala Asn Asp Val Leu Gly Tyr Tyr Lys Ile Leu Ser Glu Lys  
130 135 140

tac aag agc gat ctg gat agc atc aag aag tac atc aac gat aag cag 480

Tyr 145	Lys	Ser	Asp	Leu	Asp 150	Ser	Ile	Lys	Lys	Tyr 155	Ile	Asn	Asp	Lys	Gln 160	
gga	gag	aac	gag	aag	tac	ctg	ccc	ttc	ctg	aac	aac	atc	gag	acc	ctg	528
Gly	Glu	Asn	Glu	Lys 165	Tyr	Leu	Pro	Phe	Leu 170	Asn	Asn	Ile	Glu	Thr	Leu 175	
tac	aag	acc	gtc	aac	gat	aag	att	gat	ctg	ttc	gtg	atc	cac	ctg	gag	576
Tyr	Lys	Thr	Val 180	Asn	Asp	Lys	Ile	Asp 185	Leu	Phe	Val	Ile	His	Leu	Glu 190	
gcc	aag	gtc	ctg	cag	tac	aca	tat	gag	aag	agc	aac	gtg	gag	gtc	aag	624
Ala	Lys	Val 195	Leu	Gln	Tyr	Thr	Tyr 200	Glu	Lys	Ser	Asn	Val 205	Glu	Val	Lys	
atc	aag	gag	ctg	aat	tac	ctg	aag	acc	atc	cag	gat	aag	ctg	gcc	gat	672
Ile	Lys	Glu	Leu	Asn	Tyr	Leu 210	Lys	Thr	Ile 215	Gln	Asp	Lys 220	Leu	Ala	Asp	
ttc	aag	aag	aac	aac	aac	ttc	gtc	gga	atc	gcc	gat	ctg	agc	acc	gat	720
Phe	Lys	Lys	Asn	Asn	Asn	Phe 225	Val	Gly	Ile 230	Ala	Asp	Leu 235	Ser	Thr	Asp 240	
tac	aac	cac	aac	aac	ctg	ctg	acc	aag	ttc	ctg	agc	acc	gga	atg	gtc	768
Tyr	Asn	His	Asn	Asn	Leu 245	Leu	Thr	Lys	Phe 250	Leu	Ser	Thr	Gly	Met	Val 255	
ttc	gaa	aac	ctg	gcc	aag	acc	gtc	ctg	agc	aac	ctg	ctg	gat	gga	aac	816
Phe	Glu	Asn	Leu 260	Ala	Lys	Thr	Val	Leu 265	Ser	Asn	Leu	Leu	Asp	Gly	Asn 270	
ctg	cag	gga	atg	ctg	cag	atc	agc	cag	cac	cag	tgt	gtg	aag	aag	cag	864
Leu	Gln	Gly	Met 275	Leu	Gln	Ile	Ser	Gln	His	Gln	Cys	Val	Lys	Lys	Gln 285	
tgt	ccc	cag	aac	agc	gga	tgc	ttc	aga	cac	ctg	gat	gag	agg	gag	gag	912
Cys	Pro	Gln	Asn	Ser	Gly	Cys 290	Phe	Arg	His	Leu	Asp	Glu	Arg	Glu	Glu 300	
tgc	aag	tgc	ctg	ctg	aac	tac	aag	cag	gaa	gga	gat	aag	tgt	gtg	gaa	960
Cys	Lys	Cys	Leu	Leu	Asn	Tyr 305	Lys	Gln	Glu	Gly	Asp	Lys	Cys	Val	Glu 310	
aac	ccc	aat	cct	act	tgt	aac	gag	aac	aat	gga	gga	tgc	gat	gcc	gat	1008
Asn	Pro	Asn	Pro	Thr	Cys	Asn 325	Glu	Asn	Asn	Gly	Gly	Cys	Asp	Ala	Asp 330	
gcc	aag	tgt	acc	gag	gag	gat	tca	gga	agc	aac	gga	aag	aag	atc	acc	1056
Ala	Lys	Cys	Thr 340	Glu	Glu	Asp	Ser	Gly	Ser	Asn	Gly	Lys	Lys	Ile	Thr 345	
tgc	gag	tgt	acc	aag	cct	gat	tct	tat	cca	ctg	ttc	gat	ggt	att	ttc	1104
Cys	Glu	Cys	Thr 355	Lys	Pro	Asp	Ser	Tyr	Pro	Leu	Phe	Asp	Gly	Ile	Phe 360	
tgc	agt	cac	cac	cac	cac	cac	cac	taa	ctc	gag	gat	cc				1142
Cys	Ser	His	His	His	His	His	His	*	Leu	Glu	Asp					

370

375

&lt;210&gt; 9

&lt;211&gt; 355

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> altered MSP sequence; preferably, a bacterium,  
virus, or parasite

&lt;400&gt; 9

Ala	Val	Thr	Pro	Ser	Val	Ile	Asp	Asn	Ile	Leu	Ser	Lys	Ile	Glu	Asn
1				5				10						15	
Glu	Tyr	Glu	Val	Leu	Tyr	Leu	Lys	Pro	Leu	Ala	Gly	Val	Tyr	Arg	Ser
			20				25						30		
Leu	Lys	Lys	Gln	Leu	Glu	Asn	Asn	Val	Met	Thr	Phe	Asn	Val	Asn	Val
		35				40						45			
Lys	Asp	Ile	Leu	Asn	Ser	Arg	Phe	Asn	Lys	Arg	Glu	Asn	Phe	Lys	Asn
	50				55					60					
Val	Leu	Glu	Ser	Asp	Leu	Ile	Pro	Tyr	Lys	Asp	Leu	Thr	Ser	Ser	Asn
65				70					75					80	
Tyr	Val	Val	Lys	Asp	Pro	Tyr	Lys	Phe	Leu	Asn	Lys	Glu	Lys	Arg	Asp
			85					90						95	
Lys	Phe	Leu	Ser	Tyr	Asn	Tyr	Ile	Lys	Asp	Ser	Ile	Asp	Thr	Asp	
		100				105						110			
Ile	Asn	Phe	Ala	Asn	Asp	Val	Leu	Gly	Tyr	Tyr	Lys	Ile	Leu	Ser	Glu
		115				120						125			
Lys	Tyr	Lys	Ser	Asp	Leu	Asp	Ser	Ile	Lys	Lys	Tyr	Ile	Asn	Asp	Lys
	130				135						140				
Gln	Gly	Glu	Asn	Glu	Lys	Tyr	Leu	Pro	Phe	Leu	Asn	Asn	Ile	Glu	Thr
145				150					155					160	
Leu	Tyr	Lys	Thr	Val	Asn	Asp	Lys	Ile	Asp	Leu	Phe	Val	Ile	His	Leu
			165					170						175	
Glu	Ala	Lys	Val	Leu	Asn	Tyr	Thr	Tyr	Glu	Lys	Ser	Asn	Val	Glu	Val
		180					185					190			
Lys	Ile	Lys	Glu	Leu	Asn	Tyr	Leu	Lys	Thr	Ile	Gln	Asp	Lys	Leu	Ala
	195				200						205				
Asp	Phe	Lys	Lys	Asn	Asn	Asn	Phe	Val	Gly	Ile	Ala	Asp	Leu	Ser	Thr
	210			215					220						
Asp	Tyr	Asn	His	Asn	Asn	Leu	Leu	Thr	Lys	Phe	Leu	Ser	Thr	Gly	Met
225				230					235					240	
Val	Phe	Glu	Asn	Leu	Ala	Lys	Thr	Val	Leu	Ser	Asn	Leu	Leu	Asp	Gly
			245					250						255	
Asn	Leu	Gln	Gly	Met	Leu	Asn	Ile	Ser	Gln	His	Gln	Cys	Val	Lys	Lys
		260				265						270			
Gln	Cys	Pro	Gln	Asn	Ser	Gly	Cys	Phe	Arg	His	Leu	Asp	Glu	Arg	Glu
	275					280					285				
Glu	Cys	Lys	Cys	Leu	Leu	Asn	Tyr	Lys	Gln	Glu	Gly	Asp	Lys	Cys	Val
	290				295						300				
Glu	Asn	Pro	Asn	Pro	Thr	Cys	Asn	Glu	Asn	Asn	Gly	Gly	Cys	Asp	Ala
305				310					315					320	
Asp	Ala	Lys	Cys	Thr	Glu	Glu	Asp	Ser	Gly	Ser	Asn	Gly	Lys	Lys	Ile
			325				330						335		
Thr	Cys	Glu	Cys	Thr	Lys	Pro	Asp	Ser	Tyr	Pro	Leu	Phe	Asp	Gly	Ile
		340					345						350		



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<210> 10
<211> 361
<212> PRT
<213> Plasmodium falciparum
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Ala 1	Val	Thr	Pro	Ser 5	Val	Ile	Asp	Asn	Ile 10	Leu	Ser	Lys	Ile	Glu 15	Asn
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			20					25					30		
Leu	Lys	Lys	Gln	Leu	Glu	Asn	Asn	Val	Met	Thr	Phe	Asn	Val	Asn	Val
		35					40					45			
Lys	Asp	Ile	Leu	Asn	Ser	Arg	Phe	Asn	Lys	Arg	Glu	Asn	Phe	Lys	Asn
	50					55					60				
Val	Leu	Glu	Ser	Asp	Leu	Ile	Pro	Tyr	Lys	Asp	Leu	Thr	Ser	Ser	Asn
65				70						75					80
Tyr	Val	Val	Lys	Asp	Pro	Tyr	Lys	Phe	Leu	Asn	Lys	Glu	Lys	Arg	Asp
			85						90					95	
Lys	Phe	Leu	Ser	Ser	Tyr	Asn	Tyr	Ile	Lys	Asp	Ser	Ile	Asp	Thr	Asp
			100					105					110		
Ile	Asn	Phe	Ala	Asn	Asp	Val	Leu	Gly	Tyr	Tyr	Lys	Ile	Leu	Ser	Glu
		115					120					125			
Lys	Tyr	Lys	Ser	Asp	Leu	Asp	Ser	Ile	Lys	Lys	Tyr	Ile	Asn	Asp	Lys
	130					135					140				
Gln	Gly	Glu	Asn	Glu	Lys	Tyr	Leu	Pro	Phe	Leu	Asn	Asn	Ile	Glu	Thr
145				150						155					160
Leu	Tyr	Lys	Thr	Val	Asn	Asp	Lys	Ile	Asp	Leu	Phe	Val	Ile	His	Leu
			165						170					175	
Glu	Ala	Lys	Val	Leu	Asn	Tyr	Thr	Tyr	Glu	Lys	Ser	Asn	Val	Glu	Val
			180					185					190		
Lys	Ile	Lys	Glu	Leu	Asn	Tyr	Leu	Lys	Thr	Ile	Gln	Asp	Lys	Leu	Ala
		195					200					205			
Asp	Phe	Lys	Lys	Asn	Asn	Asn	Phe	Val	Gly	Ile	Ala	Asp	Leu	Ser	Thr
	210					215					220				
Asp	Tyr	Asn	His	Asn	Asn	Leu	Leu	Thr	Lys	Phe	Leu	Ser	Thr	Gly	Met
225				230						235					240
Val	Phe	Glu	Asn	Leu	Ala	Lys	Thr	Val	Leu	Ser	Asn	Leu	Leu	Asp	Gly
			245						250					255	
Asn	Leu	Gln	Gly	Met	Leu	Asn	Ile	Ser	Gln	His	Gln	Cys	Val	Lys	Lys
			260					265					270		
Gln	Cys	Pro	Gln	Asn	Ser	Gly	Cys	Phe	Arg	His	Leu	Asp	Glu	Arg	Glu
		275					280					285			
Glu	Cys	Lys	Cys	Leu	Leu	Asn	Tyr	Lys	Gln	Glu	Gly	Asp	Lys	Cys	Val
	290					295					300				
Glu	Asn	Pro	Asn	Pro	Thr	Cys	Asn	Glu	Asn	Asn	Gly	Gly	Cys	Asp	Ala
305				310						315					320
Asp	Ala	Lys	Cys	Thr	Glu	Glu	Asp	Ser	Gly	Ser	Asn	Gly	Lys	Lys	Ile
			325						330				335		
Thr	Cys	Glu	Cys	Thr	Lys	Pro	Asp	Ser	Tyr	Pro	Leu	Phe	Asp	Gly	Ile
			340					345					350		
Phe	Cys	Ser	His	His	His	His	His	His							

<210> 11

<211> 379  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> altered MSP sequence; preferably, a bacterium,  
 virus, or parasite

<400> 11

Met	Lys	Val	Leu	Ile	Ile	Ala	Cys	Leu	Val	Ala	Leu	Ala	Ile	Ala	Ala	1	5	10	15
Val	Thr	Pro	Ser	Val	Ile	Asp	Asn	Ile	Leu	Ser	Lys	Ile	Glu	Asn	Glu	20	25	30	
Tyr	Glu	Val	Leu	Tyr	Leu	Lys	Pro	Leu	Ala	Gly	Val	Tyr	Arg	Ser	Leu	35	40	45	
Lys	Lys	Gln	Leu	Glu	Asn	Asn	Val	Met	Thr	Phe	Asn	Val	Asn	Val	Lys	50	55	60	
Asp	Ile	Leu	Asn	Ser	Arg	Phe	Asn	Lys	Arg	Glu	Asn	Phe	Lys	Asn	Val	65	70	75	80
Leu	Glu	Ser	Asp	Leu	Ile	Pro	Tyr	Lys	Asp	Leu	Thr	Ser	Ser	Asn	Tyr	85	90	95	
Val	Val	Lys	Asp	Pro	Tyr	Lys	Phe	Leu	Asn	Lys	Glu	Lys	Arg	Asp	Lys	100	105	110	
Phe	Leu	Ser	Tyr	Asn	Tyr	Ile	Lys	Asp	Ser	Ile	Asp	Thr	Asp	Ile		115	120	125	
Asn	Phe	Ala	Asn	Asp	Val	Leu	Gly	Tyr	Tyr	Lys	Ile	Leu	Ser	Glu	Lys	130	135	140	
Tyr	Lys	Ser	Asp	Leu	Asp	Ser	Ile	Lys	Lys	Tyr	Ile	Asn	Asp	Lys	Gln	145	150	155	160
Gly	Glu	Asn	Glu	Lys	Tyr	Leu	Pro	Phe	Leu	Asn	Asn	Ile	Glu	Thr	Leu	165	170	175	
Tyr	Lys	Thr	Val	Asn	Asp	Lys	Ile	Asp	Leu	Phe	Val	Ile	His	Leu	Glu	180	185	190	
Ala	Lys	Val	Leu	Gln	Tyr	Thr	Tyr	Glu	Lys	Ser	Asn	Val	Glu	Val	Lys	195	200	205	
Ile	Lys	Glu	Leu	Asn	Tyr	Leu	Lys	Thr	Ile	Gln	Asp	Lys	Leu	Ala	Asp	210	215	220	
Phe	Lys	Lys	Asn	Asn	Asn	Phe	Val	Gly	Ile	Ala	Asp	Leu	Ser	Thr	Asp	225	230	235	240
Tyr	Asn	His	Asn	Asn	Leu	Leu	Thr	Lys	Phe	Leu	Ser	Thr	Gly	Met	Val	245	250	255	
Phe	Glu	Asn	Leu	Ala	Lys	Thr	Val	Leu	Ser	Asn	Leu	Leu	Asp	Gly	Asn	260	265	270	
Leu	Gln	Gly	Met	Leu	Gln	Ile	Ser	Gln	His	Gln	Cys	Val	Lys	Lys	Gln	275	280	285	
Cys	Pro	Gln	Asn	Ser	Gly	Cys	Phe	Arg	His	Leu	Asp	Glu	Arg	Glu	Glu	290	295	300	
Cys	Lys	Cys	Leu	Leu	Asn	Tyr	Lys	Gln	Glu	Gly	Asp	Lys	Cys	Val	Glu	305	310	315	320
Asn	Pro	Asn	Pro	Thr	Cys	Asn	Glu	Asn	Asn	Gly	Gly	Cys	Asp	Ala	Asp	325	330	335	
Ala	Lys	Cys	Thr	Glu	Glu	Asp	Ser	Gly	Ser	Asn	Gly	Lys	Lys	Ile	Thr	340	345	350	
Cys	Glu	Cys	Thr	Lys	Pro	Asp	Ser	Tyr	Pro	Leu	Phe	Asp	Gly	Ile	Phe	355	360	365	
Cys	Ser	His	His	His	His	His	His	Leu	Glu	Asp						370	375		

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